

09558421-042600

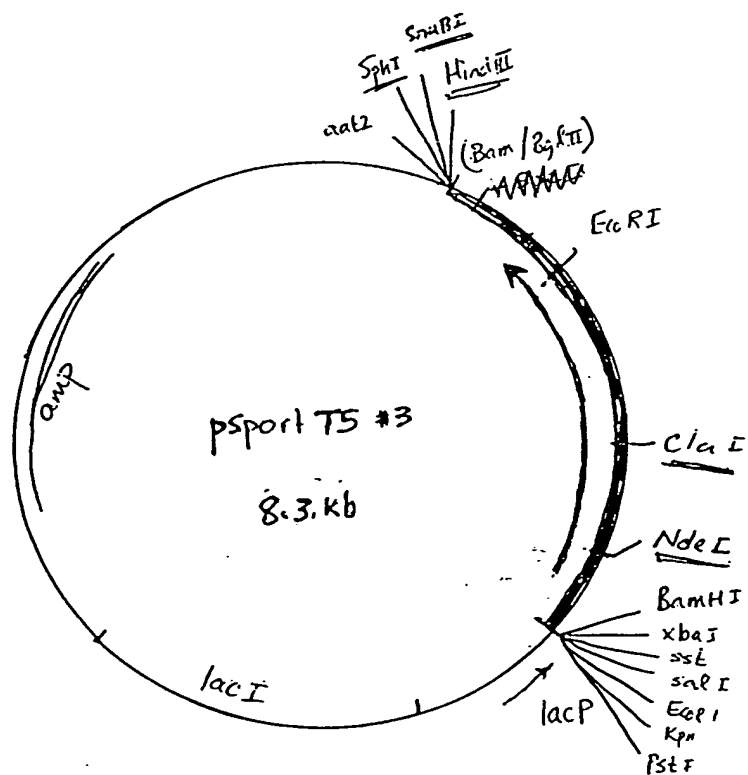


Fig. 1

09558421.042600

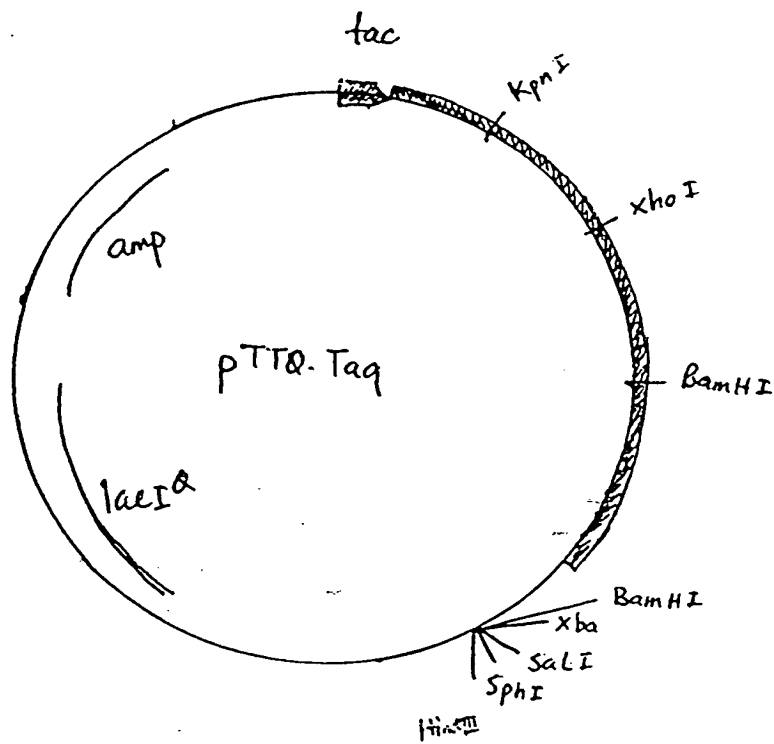
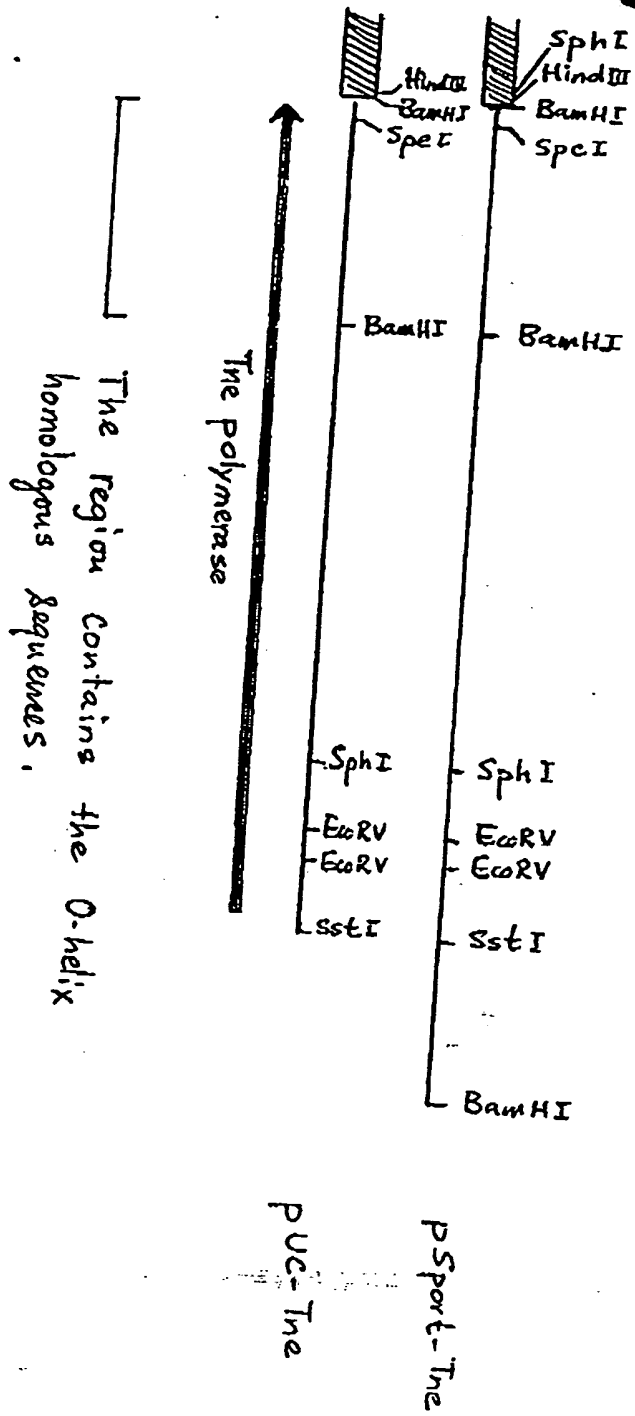


Fig. 2

Fig. 3



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*** SEQUENCE ***

BamHI

1 GGATCCAGAC TGGTGGATCG TCAGTGGCGA TTATTCCCAA ATAGAACTCA GAATCCTCGC
→ G S R L V D R Q C G L F P N R T Q N P R
D P D W W I V S A D Y S Q I E L R I L
I Q T G G S S V R I I P K - N S E S S

61 TCATCTCAGT GGTGATGAGA ACCTTGTGAA GGCCTTCGAG GAGGGCATCG ATGTGCACAC
→ S S Q W - - E P C E G L R G G H R C A H
A H L S G D E N L V K A F E E G I D V H
L I S V V M R T L - R P S R R A S M C T

121 CTGACTGCC TCCAGGATCT ACAACGTAAA GCCAGAAGAA GTCAACCAAG AAATGCCAGC
→ L D C L Q D L Q R K A R R S E R R N A T
T L T A S R I Y N V K P E E V N E E M R
P - L P P G S T T - S Q K K - T K K C D

181 GGTGGAAAG ATGGTGAAC TGTCTATAAT ATACGGTGTG ACACCGTACG GTCTTTCTGT
→ G W K D G E L L Y N I R C H T V R S F C
R V G K M V N (F) S I I Y G V T P Y G L S
G L E R W - T S L - Y T V S H R T V F L

241 GAGACTTGA ATACCGGTTA AAGAAGCAGA AAAGATGATT ATCAGCTATT TCACACTGTA
→ E T W N T G - R S R K D D Y Q L F H T V
V R L G I P V K E A E K M I I S Y F T L
- D L E Y R L K K Q K R - L S A I S H C

301 TCCAAAGGTG CGAAGCTACA TCCAGCAGGT TGTTCAGAG GCAAAAGAGA AGGGCTACGT
→ S K G A K L H P A G C C R G K R E G L R
Y P K V R S Y I Q Q V V A E A K E K G Y
I Q R C E A T S S R L L Q R Q K R R A T

361 CAGGACTCTC TTGGAAGAA AAAGAGATAT TCCCCAGGTC ATGGCAAGGG ACAAGAACAC
→ Q D S L W K K K R Y S P A H G K G Q E H
V R T L F G R K R D I P Q L M A R D K N
S G L S L E E K E I P P S S W Q G T R T

421 CCAGTCCGAA GGCGAAAGAA TCGCAATAAA CACCCCCATT CAGGGAAGTG CGGCAGATAT
→ P V R R R K N R N K H P H S G N C G R Y
T Q S E G E R I A I N T P I Q G T A A D
P S P K A K E S Q - T P P F R E L R Q I

481 AATAAAATTG GCTATGATAG ATATAGACGA GGAGCTGAGA AAAAGAAACA TGAAATCCAG
→ N K I G Y D R Y R R G A E K K K H E I Q
I I K L A M I D I D E E L R K R N M K S
- - N W L - - I - T R S - E K E T - N P

541 AATGATCATT CAGGTTTCATG ACGAACTGGT CTCGAGGTT CCCGATGAGG AAAAAGAAGA
→ N D H S G S - R T G L R G S R - G K R R
R M I I Q V H D E L V F E V P D E E K E
E - S F R F M T N W S S R F P M R K K K

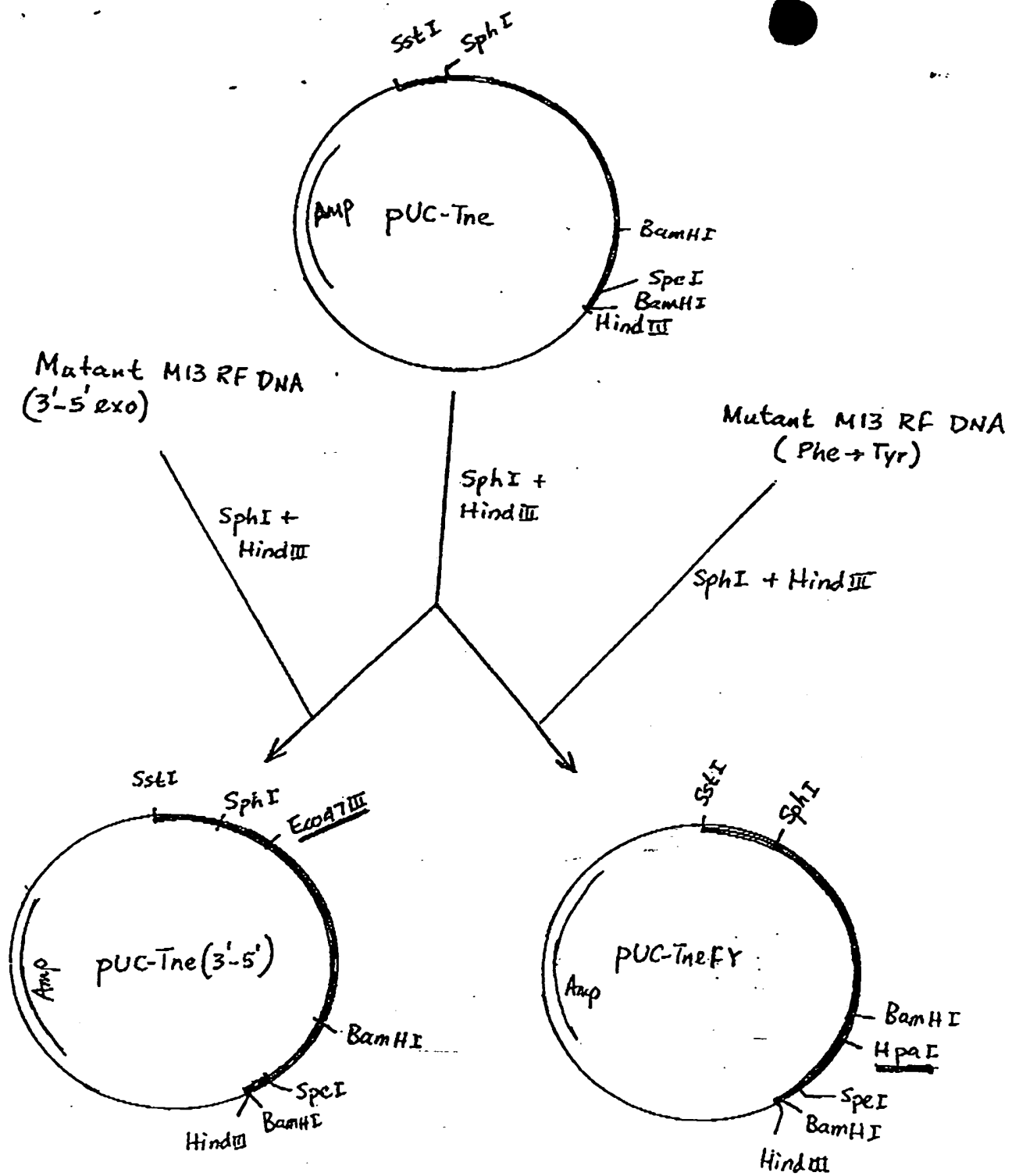
501 ACTAGTTGAT CTGGTGAAGA ACAAATGAC AAATGTGGTG AAATCTCTG TGCCTCTGA
→ T S - S G E E Q N D K C G E T L C A S -
E L V D L V K N K M T N V V K L S V P L
N - L I W - R T K - Q M W - N S L C L L

Fig 4

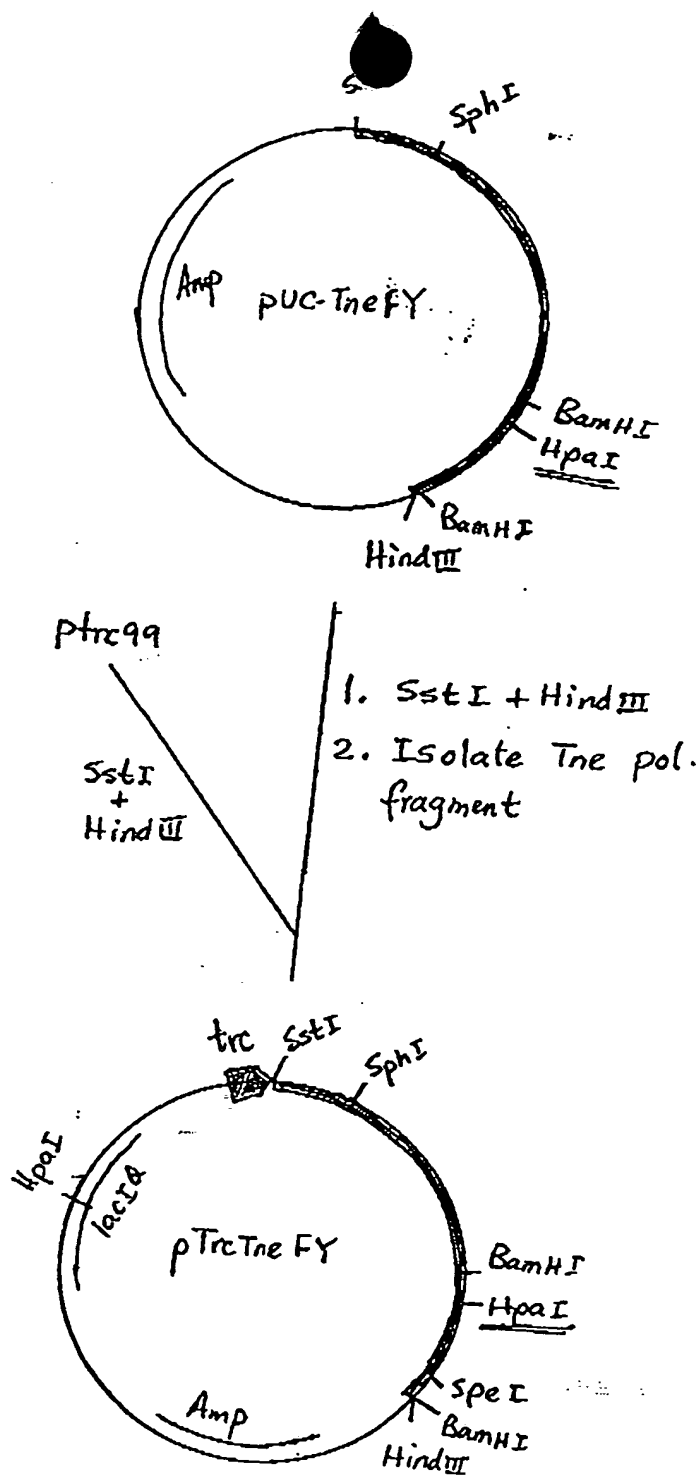
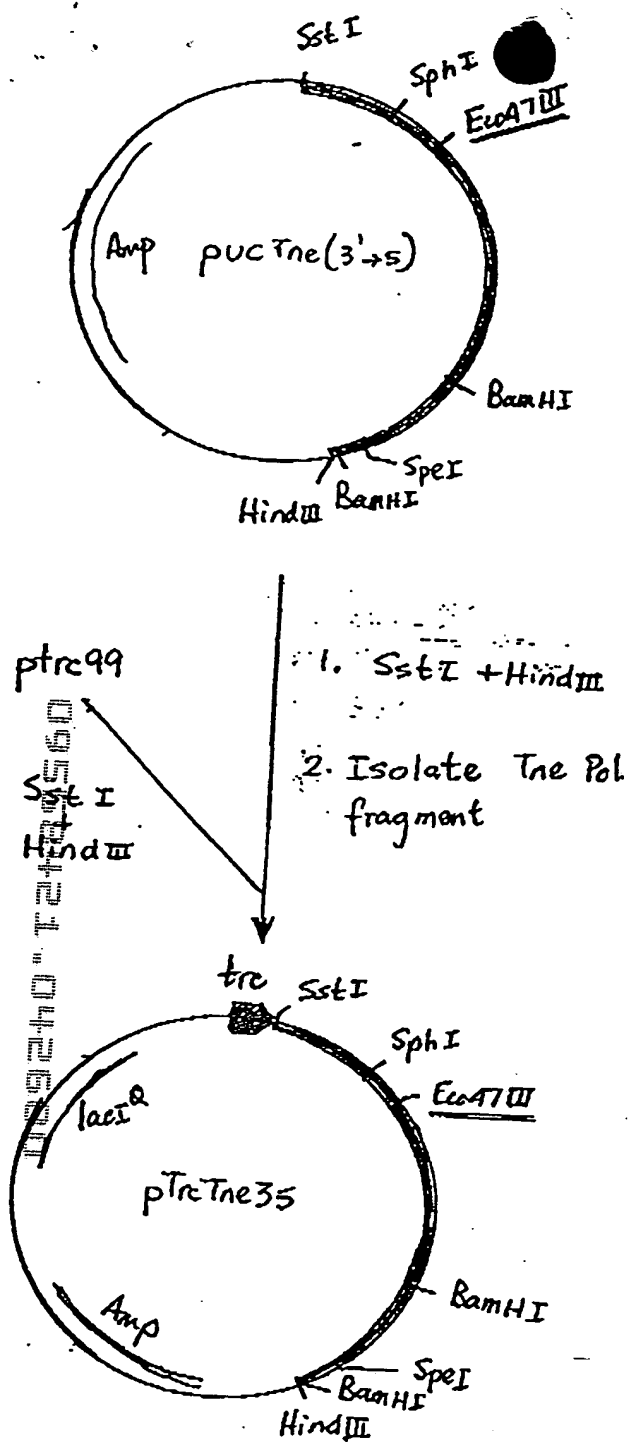
661 GGTTCACATA AGCATCGGAA AA GTC TTGA
G - H K H R K L V L
→ E V D I S I G K S W S -
R L T - A S E. K A G L

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5A
Fig. 3A



58
Fig 3B

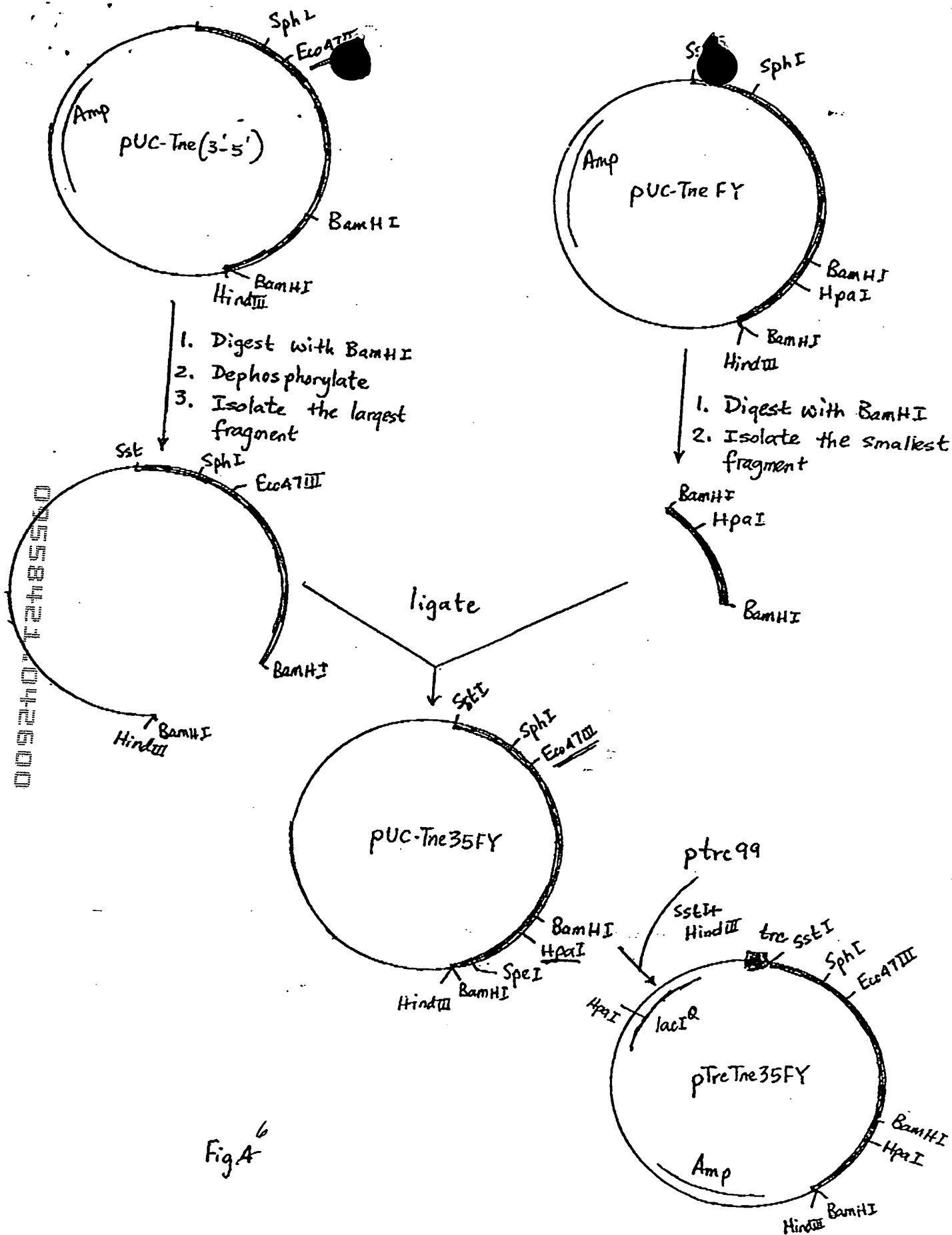
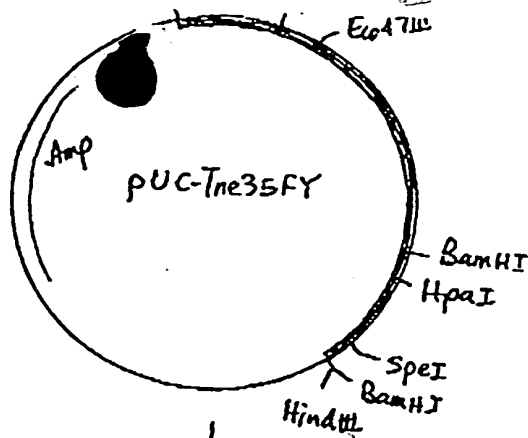
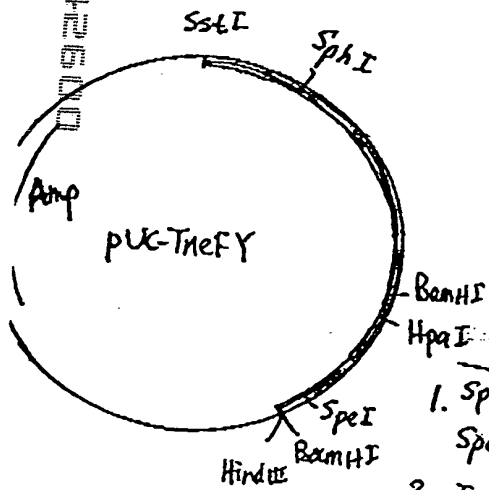
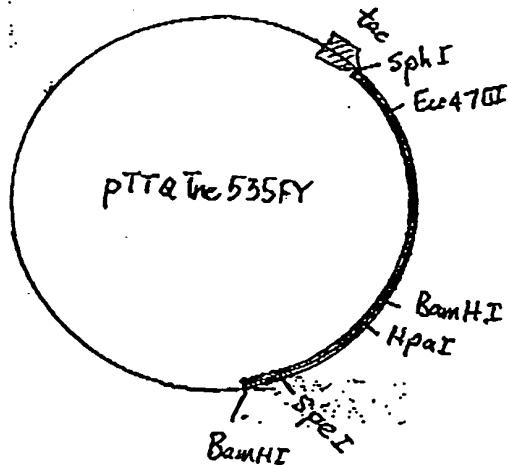


Fig 4⁶



PTTQ19 SphI+SmaI

1. Digest with HindIII
2. Fill-in
3. Digest with SphI
4. Isolate Tne pol. fragment



1. SphI + SpeI digestion
2. Isolate Vector plus small remaining Tne Pol fragment

1. SphI + SpeI digestion
2. Isolate Tne Pol fragment

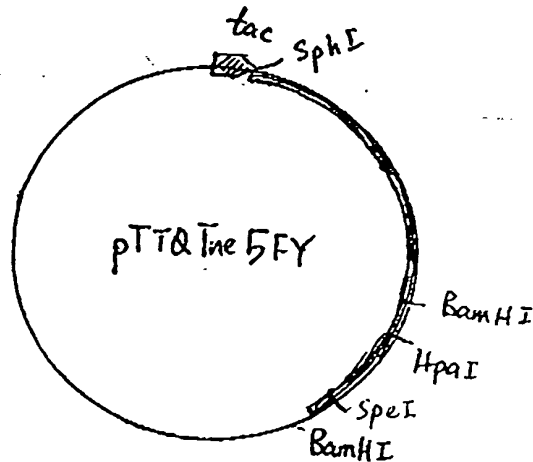


Fig. 5